

GCAGGTCATG TGGCCCCCTC TGTGGGCACC CTCTGCAGCC ACGGCCACCT GCACTCTGGG 1500
 GCCTCAGGTC CCAAGGCTGA GGCTCTGCTG CAGGAGGGTG AGCTGCTGCT ATCACCCAC 1560
 ATGCAGAAGG CACTGGAAGG TGTGCACTAC ATTGCCGACC ACCTGCGGTC TGAGGATGCT 1620
 GACTCTTCGG TGAAGGAGGA CTGGAAGTAT GTTGCCATGG TCATCGACAG GATCTTCCTC 1680
 TGGCTGTTTA TCATCGTCTG CTTCTGGGG ACCATCGGCC TCTTTCTGCC TCCGTTCTTA 1740
 GCTGGAATGA TCTGACTGCA CCTCCCTCGA GCTGGCTCCC AGGGCAAAGG GGAGGGTTCT 1800
 TGGATGTGGA AGGGCTTTGA ACAATGTTTA GATTTGGAGA TGAGCCCAA GTGCCAGGGA 1860
 GAACAGCCAG GTGAGGTGGG AGGTTGCAGA GCCAGGTGAG GTCTCTCTAA GTCAGGCTGG 1920
 GGTGAAGTT TGGAGTCTGT CCGAGTTTC AGGGTGCTGA GCTGTATGGT CCAGCAGGGG 1980
 AGTAATAAGG GCTCTTCCGG AAGGGGAGGA AGCGGGAGGC AGGGCCTGCA CCTGATGTGG 2040
 AGGTACAGGG CAGATCTTCC CTACCGGGGA GGGATGGATG GTTGGATACA GGTGGCTGGG 2100
 CTATTCCATC CATCTGGAAG CACATTGAG CCTCCAGGCT TCTCCTTGAC GTCATTCTC 2160
 TCCTTCCTTG CTCCAAATG GCTCTGCACC AGCGGGCCCC CAGGAGGTCT GGCAGAGCTG 2220
 AGAGCCATGG CCTGCAGGGG CTCCATATGT CCTACGCGT GCAGCAGGCA AACAAGA 2277

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Pro	Ser	Cys	Pro	Val	Phe	Leu	Ser	Phe	Thr	Lys	Leu	Ser	Leu
1				5					10					15	
Trp	Trp	Leu	Leu	Leu	Thr	Pro	Ala	Gly	Gly	Glu	Glu	Ala	Lys	Arg	Pro
		20						25					30		
Pro	Pro	Arg	Ala	Pro	Gly	Asp	Pro	Leu	Ser	Ser	Pro	Ser	Pro	Thr	Ala
		35					40					45			
Leu	Pro	Gln	Gly	Gly	Ser	His	Thr	Glu	Thr	Glu	Asp	Arg	Leu	Phe	Lys
	50					55					60				
His	Leu	Phe	Arg	Gly	Tyr	Asn	Arg	Trp	Ala	Arg	Pro	Val	Pro	Asn	Thr
65					70				75					80	
Ser	Asp	Val	Val	Ile	Val	Arg	Phe	Gly	Leu	Ser	Ile	Ala	Gln	Leu	Ile
			85					90						95	
Asp	Val	Asp	Glu	Lys	Asn	Gln	Met	Met	Thr	Thr	Asn	Val	Trp	Leu	Lys
		100					105						110		
Gln	Glu	Trp	Ser	Asp	Tyr	Lys	Leu	Arg	Trp	Asn	Pro	Ala	Asp	Phe	Gly
	115						120					125			
Asn	Ile	Thr	Ser	Leu	Arg	Val	Pro	Ser	Glu	Met	Ile	Trp	Ile	Pro	Asp
	130					135					140				

Tyr Ile Ala Glu Asn Met Lys Ala Gln Asn Glu Ala Lys Glu Ile Gln
450 455 460

Asp Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp
465 470 475 480

Val Phe Thr Leu Val Cys Ile Leu Gly Thr Ala Gly Leu Phe Leu Gln
485 490 495

Pro Leu Met Ala Arg Glu Asp Ala
500

(i) SEQUENCE CHARACTERISTICS:

- (11) MOLECULE TYPE: cDNA

(A) NAME/KEY: CDS

- (D) OTHER INFORMATION: /product= "ALPHA-4 SUBUNIT"

GCGCTCGCTG	CGGCGCCGCC	GCCGCNCCGC	GCGCCACAGG	AGAAGGCGAN	CCGGGCCCGG	60
CGGCCGAAGC	GGCCCCGCGAG	GCGCGGGAGG	CATGAAGTTG	GGCGCGCACG	GGCCTCGAAG	120
CGGCGGGGAG	CCGGGAGCCG	CCCGCATCTA	GAGCCCGCGA	GGTGCCTGCG	CCATGGAGCT	180
AGGGGGCCCC	GGAGCGCCGC	GGCTGCTGCC	GCCGCTGCTG	CTGCTTCTGG	GGACCGCCCT	240
CCTGCGCGCC	AGCAGCCATG	TGGAGACCCG	GGCCCCACGC	GAGGAGCGGC	TCCTGAAGAA	300
ACTCTTCTCC	GGTTACAACA	AGTGGTCCCG	ACCCGTGGCC	AACATCTCGG	ACGTGGTCTT	360
CGTCCGCTTC	GGCCTGTCCA	TCGCTCAGCT	CATTGACGTG	GATGAGAAGA	ACCAGATGAT	420
GACCACGAAC	GTCTGGGTGA	AGCAGGAGTG	GCACGACTAC	AAGCTGCGCT	GGGACCCAGC	480
TGACTATGAG	AATGTCACCT	CCATCCGCAT	CCCCTCCGAG	CTCATCTGGC	GGCCGGACAT	540
CGCCCTCTAC	AACAATGCTG	ACGGGGACTT	CGCGGCCACC	CACCTGACCA	AGGCCCACTT	600
GTTCATGAC	GGGCGGGTGC	AGCGGACTCC	CCCGGCCATT	TACAAGAGCT	CCTGCAGCAT	660
CGACGTCACC	TTCTTCCCTT	TCGACCAGCA	GAAGTGCACC	ATGAAATTCG	GCTCCTGGAC	720
CTACGACAAG	GCCAAGATCG	ACCTGGTGAA	CATGCACAGC	CGCGTGGACC	AGCTGGACTT	780
CTGGGAGAGT	GGCGAGTGGC	TCATCTCGGA	CGCCGTGGGC	ACCTACAACA	CCAGGAAGTA	840
CGAGTGCTGC	GCCGAGATCT	ACCCGGACAT	CACCTATGCC	TACGCCATCC	GGCGGCTGCC	900
GCTCTTCTAC	ACCATCAACT	TCATCATCCC	CTGGCTGCTC	ATCTCCTGCC	TCACCGCGCT	960
GGTCTTCTAC	CTGCCCTCCG	AGTGTGGCGA	GAAGATCACG	CTGTGCATCT	CCGTGCTGCT	1020
GTGCTCACC	GTCTTCCTGC	TGCTCATCAC	CGAGATCATC	CCGTCCACCT	CACTGGTCACT	1080

CCCACTCATC GCGGAGTACC TGCTGTTTAC CATGATCTTC GTCACCCTGT CCATCGCCAT 1140
 CACGGTCTTC GTGCTCAACG TGCACCACCG CTCGCCACGC ACGCACACCA TGCCACCTG 1200
 GGTACGCAGG GTCTTCCTGG ACATCGTGCC ACGCCTGCTC CTCATGAAGC GGCCGTCCGT 1260
 GGTCAAGGAC AATTGCCGGC GGCTCATCGA GTCCATGCAT AAGATGGCCA GTGCCCCGCG 1320
 CTTCTGGCCC GAGCCAGAAG GGGAGCCCCC TGCCACGAGC GGCACCCAGA GCCTGCACCC 1380
 TCCCTCACCG TCCTTCTGCG TCCCCCTGGA TGTGCCGGCT GAGCCTGGGC CTTCCTGCAA 1440
 GTCACCCTCC GACCAGCTCC CTCCTCAGCA GCCCCTGGAA GCTGAGAAAG CCAGCCCCCA 1500
 CCCCCTGCCT GGACCTGCC GCGCGCCCCA CGGCACCCAG GCACCAGGGC TGGCCAAAGC 1560
 CAGGTCCCTC AGCGTCCAGC ACATGTCCAG CCCTGGCGAA GCGGTGGAAG GCGGCGTCCG 1620
 GTGCCGGTCT CGGAGCATCC AGTACTGTGT TCCCCGAGAC GATGCCGCC CCGAGGCAGA 1680
 TGGCCAGGCT GCGGCGCCCC TGGCCTCTCG CAACAGCCAC TCGGCTGAGC TCCCACCCCC 1740
 AGACCAGCCC TCTCCGTGCA AATGCACATG CAAGAAGGAG CCCTCTTCGG TGTCCCCGAG 1800
 CGCCACGGTC AAGACCCGCA GCACCAAAGC GCGCGCGCCG CACCTGCCCC TGTGCGCGGC 1860
 CCTGAGCCCG GCGGTGGAGG GCGTCCAGTA CATTGCAGAC CACCTGAAGG CCGAAGACAC 1920
 AGACTTCTCG GTGAAGGAGG ACTGGAAGTA CGTGCCCATG GTCATCGACC GCATCTTCTT 1980
 CTGGATGTTT ATCATCGTCT GCCTGCTGGG GACGGTGGGC CTCTTCCTGC CGCCCTGGCT 2040
 GGCTGGCATG ATCTAGGAAG GGACCGGGAG CCTGCGTGGC CTGGGGCTGC CGYGCACGGG 2100
 GCCAGCATCC ATGCGGCCGG CCTGGGGCCG GGCTGGCTTC TCCCTGGACT CTGTGGGGCC 2160
 ACACGTTTGC CAAATTTTCC TTCCTGTCTT GTGTCTGCTG TAAGACGGCC TTGGACGGCG 2220
 ACACGGCCTC TGGGGAGACC GAGTGTGGAG CTGCTTCCAG TTGGACTCTS GCCTCAGNAG 2280
 GCAGCGGCTT GGAGCAGAGG TGGCGGTGCG CGCCTYCTAC CTGCAGGACT CGGGCTAAGT 2340
 CCAGCTCTCC CCCTGCGCAG CCC 2363

(2) INFORMATION FOR SEQ ID NO:6:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 627 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Leu Gly Gly Pro Gly Ala Pro Arg Leu Leu Pro Pro Leu Leu
 1 5 10 15
 Leu Leu Leu Gly Thr Gly Leu Leu Arg Ala Ser Ser His Val Glu Thr
 20 25 30
 Arg Ala His Ala Glu Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr
 35 40 45
 Asn Lys Trp Ser Arg Pro Val Ala Asn Ile Ser Asp Val Val Leu Val
 50 55 60

CCF = FSCC260

Glu Pro Gly Pro Ser Cys Lys Ser Pro Ser Asp Gln Leu Pro Pro Gln
420 425 430

Gln Pro Leu Glu Ala Glu Lys Ala Ser Pro His Pro Ser Pro Gly Pr
435 440 445

Cys Arg Pro Pro His Gly Thr Gln Ala Pro Gly Leu Ala Lys Ala Arg
450 455 460

Ser Leu Ser Val Gln His Met Ser Ser Pro Gly Glu Ala Val Glu Gly
465 470 475 480

Gly Val Arg Cys Arg Ser Arg Ser Ile Gln Tyr Cys Val Pro Arg Asp
485 490 495

Asp Ala Ala Pro Glu Ala Asp Gly Gln Ala Ala Gly Ala Leu Ala Ser
500 505 510

Arg Asn Ser His Ser Ala Glu Leu Pro Pro Pro Asp Gln Pro Ser Pro
515 520 525

Cys Lys Cys Thr Cys Lys Lys Glu Pro Ser Ser Val Ser Pro Ser Ala
530 535 540

Thr Val Lys Thr Arg Ser Thr Lys Ala Pro Pro Pro His Leu Pro Leu
545 550 555 560

Ser Pro Ala Leu Ser Arg Ala Val Glu Gly Val Gln Tyr Ile Ala Asp
565 570 575

His Leu Lys Ala Glu Asp Thr Asp Phe Ser Val Lys Glu Asp Trp Lys
580 585 590

Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile
595 600 605

Val Cys Leu Leu Gly Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala
610 615 620

Gly Met Ile
625

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 155..1561
- (D) OTHER INFORMATION: /product= "ALPHA-5 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCGCGCGGA GCTGTGCGCG GGAGCGGCCC CGCTGCTGCG TGTGCCCTCG TTTGTCTCA	60
CGACTCACAC TCAGTGCTGC ATTCCCCAAG AGTTCGCGTT CCCCAGCGCG CGGTGAGAG	120
GCGGCTGCCC GCGGTCCCGC GCGGGCGCGG GGCG ATG GCG GCG CGG GGG TCA	172
Met Ala Ala Arg Gly Ser	
1 5	

GGG CCC CGC GCG CTC CGC CTG CTG CTC TTG GTC CAG CTG GTC GCG GGG Gly Pro Arg Ala Leu Arg Leu L u Leu Leu Val Gln Leu Val Ala Gly	220
CGC TGC GGT CTA GCG GGC GCG GCG GCG GCG GCG CAG AGA GGA TTA TCT Arg Cys Gly Leu Ala Gly Ala Ala Gly Gly Ala Gln Arg Gly Leu Ser	268
GAA CCT TCT TCT ATT GCA AAA CAT GAA GAT AGT TTG CTT AAG GAT TTA Glu Pro Ser Ser Ile Ala Lys His Glu Asp Ser Leu Leu Lys Asp Leu	316
TTT CAA GAC TAC GAA AGA TGG GTT CGT CCT GTG GAA CAC CTG AAT GAC Phe Gln Asp Tyr Glu Arg Trp Val Arg Pro Val Glu His Leu Asn Asp	364
AAA ATA AAA ATA AAA TTT GGA CTT GCA ATA TCT CAA TTG GTG GAT GTG Lys Ile Lys Ile Lys Phe Gly Leu Ala Ile Ser Gln Leu Val Asp Val	412
GAT GAG AAA AAT CAG TTA ATG ACA ACA AAC GTC TGG TTG AAA CAG GAA Asp Glu Lys Asn Gln Leu Met Thr Thr Asn Val Trp Leu Lys Gln Glu	460
TGG ATA GAT GTA AAA TTA AGA TGG AAC CCT GAT GAC TAT GGT GGA ATA Trp Ile Asp Val Lys Leu Arg Trp Asn Pro Asp Asp Tyr Gly Gly Ile	508
AAA GTT ATA CGT GTT CCT TCA GAC TCT GTC TGG ACA CCA GAC ATC GTT Lys Val Ile Arg Val Pro Ser Asp Ser Val Trp Thr Pro Asp Ile Val	556
TTG TTT GAT AAT GCA GAT GGA CGT TTT GAA GGG ACC AGT ACG AAA ACA Leu Phe Asp Asn Ala Asp Gly Arg Phe Glu Gly Thr Ser Thr Lys Thr	604
GTC ATC AGG TAC AAT GGC ACT GTC ACC TGG ACT CCA CCG GCA AAC TAC Val Ile Arg Tyr Asn Gly Thr Val Thr Trp Thr Pro Pro Ala Asn Tyr	652
AAA AGT TCC TGT ACC ATA GAT GTC ACG TTT TTC CCA TTT GAC CTT CAG Lys Ser Ser Cys Thr Ile Asp Val Thr Phe Phe Pro Phe Asp Leu Gln	700
AAC TGT TCC ATG AAA TTT GGT TCT TGG ACT TAT GAT GGA TCA CAG GTT Asn Cys Ser Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly Ser Gln Val	748
GAT ATA ATT CTA GAG GAC CAA GAT GTA GAC AAG AGA GAT TTT TTT GAT Asp Ile Ile Leu Glu Asp Gln Asp Val Asp Lys Arg Asp Phe Phe Asp	796
AAT GGA GAA TGG GAG ATT GTG AGT GCA ACA GGG AGC AAA GGA AAC AGA Asn Gly Glu Trp Glu Ile Val Ser Ala Thr Gly Ser Lys Gly Asn Arg	844
ACC GAC AGC TGT TGC TGG TAT CCG TAT GTC ACT TAC TCA TTT GTA ATC Thr Asp Ser Cys Cys Trp Tyr Pro Tyr Val Thr Tyr Ser Phe Val Ile	892
AAG CGC CTG CCT CTC TTT TAT ACC TTG TTC CTT ATA ATA CCC TGT ATT Lys Arg Leu Pro Leu Phe Tyr Thr Leu Phe Leu Ile Ile Pro Cys Ile	940
GGG CTC TCA TTT TTA ACT GTA CTT GTC TTC TAT CTT CCT TCA AAT GAA Gly Leu Ser Phe Leu Thr Val Leu Val Ph Tyr Leu Pro Ser Asn Glu	988

00703034 = 1566260

GGT GAA AAG ATT TGT CTC TGC ACT TCA GTA CTT GTG TCT TTG ACT GTC Gly Glu Lys Ile Cys Leu Cys Thr Ser Val Leu Val Ser Leu Thr Val 280 285 290	1036
TTC CTT CTG GTT ATT GAA GAG ATC ATA CCA TCA TCT TCA AAA GTC ATA Phe Leu Leu Val Ile Glu Glu Ile Ile Pro Ser Ser Ser Lys Val Ile 295 300 305 310	1084
CCT CTA ATT GGA GAG TAT CTG GTA TTT ACC ATG ATT TTT GTG ACA CTG Pro Leu Ile Gly Glu Tyr Leu Val Phe Thr Met Ile Phe Val Thr Leu 315 320 325	1132
TCA ATT ATG GTA ACC GTC TTC GCT ATC AAC ATT CAT CAT CGT TCT TCC Ser Ile Met Val Thr Val Phe Ala Ile Asn Ile His His Arg Ser Ser 330 335 340	1180
TCA ACA CAT AAT GCC ATG GCG CCT TTG GTC CGC AAG ATA TTT CTT CAC Ser Thr His Asn Ala Met Ala Pro Leu Val Arg Lys Ile Phe Leu His 345 350 355	1228
ACG CTT CCC AAA CTG CTT TGC ATG AGA AGT CAT GTA GAC AGG TAC TTC Thr Leu Pro Lys Leu Leu Cys Met Arg Ser His Val Asp Arg Tyr Phe 360 365 370	1276
ACT CAG AAA GAG GAA ACT GAG AGT GGT AGT GGA CCA AAA TCT TCT AGA Thr Gln Lys Glu Glu Thr Glu Ser Gly Ser Gly Pro Lys Ser Ser Arg 375 380 385 390	1324
AAC ACA TTG GAA GCT GCG CTC AAT TCT ATT CGC TAC ATT ACA AGA CAC Asn Thr Leu Glu Ala Ala Leu Asn Ser Ile Arg Tyr Ile Thr Arg His 395 400 405	1372
ATC ATG AAG GAA AAT GAT GTC CGT GAG GTT GTT GAA GAT TGG AAA TTC Ile Met Lys Glu Asn Asp Val Arg Glu Val Val Glu Asp Trp Lys Phe 410 415 420	1420
ATA GCC CAG GTT CTT GAT CGG ATG TTT CTG TGG ACT TTT CTT TTC GTT Ile Ala Gln Val Leu Asp Arg Met Phe Leu Trp Thr Phe Leu Phe Val 425 430 435	1468
TCA ATT GTT GGA TCT CTT GGG CTT TTT GTT CCT GTT ATT TAT AAA TGG Ser Ile Val Gly Ser Leu Gly Leu Phe Val Pro Val Ile Tyr Lys Trp 440 445 450	1516
GCA AAT ATA TTA ATA CCA GTT CAT ATT GGA AAT GCA AAT AAG TGAAGCCTCC Ala Asn Ile Leu Ile Pro Val His Ile Gly Asn Ala Asn Lys 455 460 465	1568
CAAGGGACTG AAGTATACAT TTAGTTAACA CACATATATC TGATGGCACC TATAAAATTA	1628
TGAAAATGTA AGTTATGTGT TAAATTTAGT GCAAGCTTTA ACAGACTAAG TTGCTAACCT	1688
CAATTTATGT TAACAGATGA TCCATTTGAA CAGTTGGCTG TATGACTGAA GTAATAACTG	1748
ATGAGATACA TTTGATCTTG TAAAAATAGC AAAATATTAT CTGAACTGGA CTAGTGAAAA	1808
ATCTAGTATT TGTATCCTGG	1828

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Year	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

Met	Ala	Ala	Arg	Gly	Ser	Gly	Pro	Arg	Ala	Leu	Arg	Leu	Leu	Leu	L	u
1				5					10						15	
Val	Gln	Leu	Val	Ala	Gly	Arg	Cys	Gly	Leu	Ala	Gly	Ala	Ala	Gly	Gly	
			20					25					30			
Ala	Gln	Arg	Gly	Leu	Ser	Glu	Pro	Ser	Ser	Ile	Ala	Lys	His	Glu	Asp	
		35					40					45				
Ser	Leu	Leu	Lys	Asp	Leu	Phe	Gln	Asp	Tyr	Glu	Arg	Trp	Val	Arg	Pro	
	50					55					60					
Val	Glu	His	Leu	Asn	Asp	Lys	Ile	Lys	Ile	Lys	Phe	Gly	Leu	Ala	Ile	
	65				70					75					80	
Ser	Gln	Leu	Val	Asp	Val	Asp	Glu	Lys	Asn	Gln	Leu	Met	Thr	Thr	Asn	
				85					90						95	
Val	Trp	Leu	Lys	Gln	Glu	Trp	Ile	Asp	Val	Lys	Leu	Arg	Trp	Asn	Pro	
		100						105					110			
Asp	Asp	Tyr	Gly	Gly	Ile	Lys	Val	Ile	Arg	Val	Pro	Ser	Asp	Ser	Val	
		115					120					125				
Trp	Thr	Pro	Asp	Ile	Val	Leu	Phe	Asp	Asn	Ala	Asp	Gly	Arg	Phe	Glu	
	130					135					140					
Gly	Thr	Ser	Thr	Lys	Thr	Val	Ile	Arg	Tyr	Asn	Gly	Thr	Val	Thr	Trp	
	145				150					155					160	
Thr	Pro	Pro	Ala	Asn	Tyr	Lys	Ser	Ser	Cys	Thr	Ile	Asp	Val	Thr	Phe	
				165					170					175		
Phe	Pro	Phe	Asp	Leu	Gln	Asn	Cys	Ser	Met	Lys	Phe	Gly	Ser	Trp	Thr	
			180					185					190			
Tyr	Asp	Gly	Ser	Gln	Val	Asp	Ile	Ile	Leu	Glu	Asp	Gln	Asp	Val	Asp	
		195					200					205				
Lys	Arg	Asp	Phe	Phe	Asp	Asn	Gly	Glu	Trp	Glu	Ile	Val	Ser	Ala	Thr	
	210					215					220					
Gly	Ser	Lys	Gly	Asn	Arg	Thr	Asp	Ser	Cys	Cys	Trp	Tyr	Pro	Tyr	Val	
	225			230						235					240	
Thr	Tyr	Ser	Phe	Val	Ile	Lys	Arg	Leu	Pro	Leu	Phe	Tyr	Thr	Leu	Phe	
				245					250					255		
Leu	Ile	Ile	Pro	Cys	Ile	Gly	Leu	Ser	Phe	Leu	Thr	Val	Leu	Val	Phe	
			260					265					270			
Tyr	Leu	Pro	Ser	Asn	Glu	Gly	Glu	Lys	Ile	Cys	Leu	Cys	Thr	Ser	Val	
		275					280					285				
Leu	Val	Ser	Leu	Thr	Val	Phe	Leu	Leu	Val	Ile	Glu	Glu	Ile	Ile	Pro	
	290					295					300					
Ser	Ser	Ser	Lys	Val	Ile	Pro	Leu	Ile	Gly	Glu	Tyr	Leu	Val	Phe	Thr	
					310					315					320	
Met	Ile	Phe	Val	Thr	Leu	Ser	Ile	Met	Val	Thr	Val	Phe				

GAA Glu 75	GTA Val	AAC Asn	CAG Gln	ATC Ile	ATG Met 80	GAA Glu	ACC Thr	AAT Asn	TTG Leu	TGG Trp 85	CTG Leu	CGT Arg	CAC His	ATC Ile	TGG Trp 90	412
AAT Asn	GAT Asp	TAT Tyr	AAA Lys 95	TTG Leu	CGC Arg	TGG Trp	GAT Asp	CCA Pro	ATG Met 100	GAA Glu	TAT Tyr	GAT Asp	GGC Gly	ATT Ile 105	GAG Glu	460
ACT Thr	CTT Leu	CGC Arg	GTT Val 110	CCT Pro	GCA Ala	GAT Asp	AAG Lys	ATT Ile 115	TGG Trp	AAG Lys	CCC Pro	GAC Asp	ATT Ile 120	GTT Val	CTC Leu	508
TAT Tyr	AAC Asn 125	AAT Asn	GCT Ala	GTT Val	GGT Gly	GAC Asp	TTC Phe 130	CAA Gln	GTA Val	GAA Glu	GGC Gly	AAA Lys 135	ACA Thr	AAA Lys	GCT Ala	556
CTT Leu 140	CTT Leu	AAA Lys	TAC Tyr	AAT Asn	GGC Gly	ATG Met 145	ATA Ile	ACC Thr	TGG Trp	ACT Thr	CCA Pro 150	CCA Pro	GCT Ala	ATT Ile	TTT Phe	604
AAG Lys 155	AGT Ser	TCC Ser	TGC Cys	CCT Pro	ATG Met 160	GAT Asp	ATC Ile	ACC Thr	TTT Phe	TTC Phe 165	CCT Pro	TTT Phe	GAT Asp	CAT His	CAA Gln 170	652
AAC Asn	TGT Cys	TCC Ser	CTA Leu 175	AAA Lys	TTT Phe	GGT Gly	TCC Ser	TGG Trp	ACG Thr 180	TAT Tyr	GAC Asp	AAA Lys	GCT Ala	GAA Glu 185	ATT Ile	700
GAT Asp	CTT Leu	CTA Leu 190	ATC Ile	ATT Ile	GGA Gly	TCA Ser	AAA Lys	GTG Val 195	GAT Asp	ATG Met	AAT Asn	GAT Asp	TTT Phe 200	TGG Trp	GAA Glu	748
AAC Asn	AGT Ser 205	GAA Glu	TGG Trp	GAA Glu	ATC Ile	ATT Ile	GAT Asp 210	GCC Ala	TCT Ser	GGC Gly	TAC Tyr	AAA Lys 215	CAT His	GAC Asp	ATC Ile	796
AAA Lys 220	TAC Tyr	AAC Asn	TGT Cys	TGT Cys	GAA Glu 225	GAG Glu	ATA Ile	TAC Tyr	ACA Thr	GAT Asp 230	ATA Ile	ACC Thr	TAT Tyr	TCT Ser	TTC Phe	844
TAC Tyr 235	ATT Ile	AGA Arg	AGA Arg	TTG Leu	CCG Pro 240	ATG Met	TTT Phe	TAC Tyr	ACG Thr	ATT Ile 245	AAT Asn	CTG Leu	ATC Ile	ATC Ile	CCT Pro 250	892
TGT Cys	CTC Leu	TTT Phe	ATT Ile	TCA Ser 255	TTT Phe	CTA Leu	ACC Thr	GTG Val 260	TTG Leu	GTC Val	TTT Phe	TAC Tyr	CTT Leu	CCT Pro 265	TCG Ser	940
GAC Asp	TGT Cys	GGT Gly	GAA Glu 270	AAA Lys	GTG Val	ACG Thr	CTT Leu	TGT Cys 275	ATT Ile	TCA Ser	GTC Val	CTG Leu	CTT Leu 280	TCT Ser	CTG Leu	988
ACT Thr	GTG Val	TTT Phe 285	TTG Leu	CTG Leu	GTC Val	ATC Ile	ACA Thr 290	GAA Glu	ACC Thr	ATC Ile	CCA Pro	TCC Ser 295	ACA Thr	TCT Ser	CTG Leu	1036
GTG Val 300	GTC Val	CCA Pro	CTG Leu	GTG Val	GGT Gly	GAG Glu 305	TAC Tyr	CTG Leu	CTG Leu	TTC Phe 310	ACC Thr	ATG Met	ATC Ile	TTT Phe	GTC Val	1084
ACA Thr 315	CTG Leu	TCC Ser	ATC Ile	GTG Val 320	GTG Val	ACT Thr	GTG Val	TTT Phe	GTG Val	TTG Leu 325	AAC Asn	ATA Ile	CAC His	TAC Tyr	CGC Arg 330	1132
ACC Thr	CCA Pro	ACC Thr	ACG Thr	CAC His 335	ACA Thr	ATG Met	CCC Pro	AGG Arg	TGG Trp 340	GTG Val	AAG Lys	ACA Thr	GTT Val	TTC Phe 345	CTG Leu	1180

AAG CTG CTG CCC CAG GTC CTG CTG ATG AGG TGG CCT CTG GAC AAG ACA	1228
Lys Leu Leu Pro Gln Val Leu Leu Met Arg Trp Pro Leu Asp Lys Thr	
350 355 360	
AGG GGC ACA GGC TCT GAT GCA GTG CCC AGA GGC CTT GCC AGG AGG CCT	1276
Arg Gly Thr Gly Ser Asp Ala Val Pro Arg Gly Leu Ala Arg Arg Pro	
365 370 375	
GCC AAA GGC AAG CTT GCA AGC CAT GGG GAA CCC AGA CAT CTT AAA GAA	1324
Ala Lys Gly Lys Leu Ala Ser His Gly Glu Pro Arg His Leu Lys Glu	
380 385 390	
TGC TTC CAT TGT CAC AAA TCA AAT GAG CTT GCC ACA AGC AAG AGA AGA	1372
Cys Phe His Cys His Lys Ser Asn Glu Leu Ala Thr Ser Lys Arg Arg	
395 400 405 410	
TTA AGT CAT CAG CCA TTA CAG TGG GTG GTG GAA AAT TCG GAG CAC TCG	1420
Leu Ser His Gln Pro Leu Gln Trp Val Val Glu Asn Ser Glu His Ser	
415 420 425	
CCT GAA GTT GAA GAT GTG ATT AAC AGT GTT CAG TTC ATA GCA GAA AAC	1468
Pro Glu Val Glu Asp Val Ile Asn Ser Val Gln Phe Ile Ala Glu Asn	
430 435 440	
ATG AAG AGC CAC AAT GAA ACC AAG GAG GTA GAA GAT GAC TGG AAA TAC	1516
Met Lys Ser His Asn Glu Thr Lys Glu Val Glu Asp Asp Trp Lys Tyr	
445 450 455	
GTG GCC ATG GTG GTG GAC AGA GTA TTT CTT TGG GTA TTT ATA ATT GTC	1564
Val Ala Met Val Val Asp Arg Val Phe Leu Trp Val Phe Ile Ile Val	
460 465 470	
TGT GTA TTT GGA ACT GCA GGG CTA TTT CTA CAG CCA CTA CTT GGG AAC	1612
Cys Val Phe Gly Thr Ala Gly Leu Phe Leu Gln Pro Leu Leu Gly Asn	
475 480 485 490	
ACA GGA AAA TCT TAAATGTAT TTTCTTTTAT GTTCAGAAAT TTACAGACAC	1664
Thr Gly Lys Ser	
495	
CATATTTGTT CTGCATTCCC TGCCACAAGG AAAGGAAAGC AAAGGCTTCC CACCCAGTC	1724
CCCCATCTGC TAAACCCG	1743

(2) INFORMATION FOR SEQ ID NO:10:

(ii) MOLECULE TYPE: protein

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Met  Leu  Thr  Ser  Lys  Gly  Gln  Gly  Phe  Leu  His  Gly  Gly  Leu  Cys  Leu
 1          5          10          15
Trp  Leu  Cys  Val  Phe  Thr  Pro  Phe  Phe  Lys  Gly  Cys  Val  Gly  Cys  Ala
          20          25          30
Thr  Glu  Glu  Arg  Leu  Phe  His  Lys  Leu  Phe  Ser  His  Tyr  Asn  Gln  Phe
          35          40          45
Ile  Arg  Pro  Val  Glu  Asn  Val  Ser  Asp  Pro  Val  Thr  Val  His  Ph  Glu
 50          55          60

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Gln Trp Val Val Glu Asn Ser Glu His Ser Pro Glu Val Glu Asp Val
420 425 430
Ile Asn Ser Val Gln Phe Ile Ala Glu Asn Met Lys Ser His Asn Glu
435 440 445
Thr Lys Glu Val Glu Asp Asp Trp Lys Tyr Val Ala Met Val Val Asp
450 455 460
Arg Val Phe Leu Trp Val Phe Ile Ile Val Cys Val Phe Gly Thr Ala
465 470 475 480
Gly Leu Phe Leu Gln Pro Leu Leu Gly Asn Thr Gly Lys Ser
485 490

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 73..1581
- (D) OTHER INFORMATION: /product= "ALPHA-7 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCGCAGGC GCAGGCCCGG GCGACAGCCG AGACGTGGAG CGCGCCGGCT CGCTGCAGCT	60
CCGGGACTCA ACATGCGCTG CTCGCCGGA GCGCTCTGGC TGGCGCTGGC CGCGTCGCTC	120
CTGCACGTGT CCCTGCAAGG CGAGTTCCAG AGGAAGCTTT ACAAGGAGCT GGTCAAGAAC	180
TACAATCCCT TGGAGAGGCC CGTGGCCAAT GACTCGCAAC CACTCACCCT CTACTTCTCC	240
CTGAGCCTCC TGCAGATCAT GGACGTGGAT GAGAAGAACC AAGTTTTAAC CACCAACATT	300
TGGCTGCAAA TGTCTTGAC AGATCACTAT TTACAGTGA ATGTGTCAGA ATATCCAGGG	360
GTGAAGACTG TTCGTTTCCC AGATGGCCAG ATTGGAAC CAGACATTCT TCTCTATAAC	420
AGTGCTGATG AGCGCTTTGA CGCCACATTC CACACTAAG TGTGGTGAA TTCTTCTGGG	480
CATTGCCAGT ACCTGCCTCC AGGCATATTC AAGAGTTCTT GCTACATCGA TGTACGCTGG	540
TTTCCCTTTG ATGTGCAGCA CTGCAAACTG AAGTTTGGGT CCTGGTCTTA CGGAGGCTGG	600
TCCTTGGATC TGCAGATGCA GGAGGCAGAT ATCAGTGGCT ATATCCCCAA TGGAGAATGG	660
GACCTAGTGG GAATCCCCGG CAAGAGGAGT GAAAGGTTCT ATGAGTGCTG CAAAGAGCCC	720
TACCCCGATG TCACCTTCAC AGTGACCATG CGCCGCAGGA CGCTCTACTA TGGCCTCAAC	780
CTGCTGATCC CCTGTGTGCT CATCTCCGCC CTCGCCCTGC TGGTGTTCCT GCTTCCTGCA	840
GATTCCGGGG AGAAGATTTC CCTGGGGATA ACAGTCTTAC TCTCTCTTAC CGTCTTCATG	900
CTGCTCGTGG CTGAGATCAT GCGCGCAACA TCCGATTCGG TACCATTGAT AGCCCACTAC	960
TTGCCAGCA CCATGATCAT CGTGGCCCTC TCGGTGGTGG TGACGGTGAT CGTGCTGCAG	1020

TACCACCACC	ACGACCCCGA	CGGGGGCAAG	ATGCCCAAGT	GGACCAGAGT	CATCCTTCTG	1080
AACTGGTGCG	CGTGGTTCTT	SCGAATGAAG	AGGCCCGGGG	AGGACAAGGT	GCGCCCGGCC	1140
TGCCAGCACA	AGCAGCGGCG	CTGCAGCCTG	GCCAGTGTGG	AGATGAGCGC	CGTGGCGCCG	1200
CCGCCCCGCA	GCAACGGGAA	CCTGCTGTAC	ATCGGCTTCC	GCGGCCTGGA	CGGCGTGCAC	1260
TGTGTCCCGA	CCCCCGACTC	TGGGGTAGTG	TGTGGCCGCA	TGGCCTGTCT	CCCCACGCAC	1320
GATGAGCACC	TCCTGCACGG	CGGGCAACCC	CCCGAGGGGG	ACCCGGACTT	GGCCAAGATC	1380
CTGGAGGAGG	TCCGCTACAT	TGCCAATCGC	TTCCGCTGCC	AGGACGAAAG	CGAGGCGGTC	1440
TGCAGCGAGT	GGAAGTTGCG	CGCCTGTGTG	GTGGACCGCC	TGTGCCTCAT	GGCCTTCTCG	1500
GTCTTCACCA	TCATCTGCAC	CATCGGCATC	CTGATGTCGG	CTCCCAACTT	CGTGGAGGCC	1560
GTGTCCAAAG	ACTTTGCGTA	ACCACGCCTG	GTTCTGTACA	TGTGGAAAAC	TCACAGATGG	1620
GCAAGGCCTT	TGGCTTGGCG	AGATTTGGGG	GTGCTAATCC	AGGACAGCAT	TACACGCCAC	1680
AACTCCAGTG	TTCCCTTCTG	GCTGTCAGTC	GTGTTGCTTA	CGGTTTCTTT	GTTACTTTAG	1740
GTAGTAGAAT	CTCAGCACTT	TGTTTCATAT	TCTCAGATGG	GCTGATAGAT	ATCCTTGGCA	1800
CATCCGTACC	ATCGGTCAGC	AGGGCCACTG	AGTAGTCATT	TTGCCCATTA	GCCCACTGCC	1860
TGGAAAGCCC	TTCGGA					1876

(2) INFORMATION FOR SEQ ID NO:12:

(ii) MOLECULE TYPE: protein

Met	Arg	Cys	Ser	Pro	Gly	Gly	Val	Trp	Leu	Ala	Leu	Ala	Ala	Ser	Leu
1			5						10					15	
Leu	His	Val	Ser	Leu	Gln	Gly	Glu	Phe	Gln	Arg	Lys	Leu	Tyr	Lys	Glu
			20					25					30		
Leu	Val	Lys	Asn	Tyr	Asn	Pro	Leu	Glu	Arg	Pro	Val	Ala	Asn	Asp	Ser
		35					40					45			
Gln	Pro	Leu	Thr	Val	Tyr	Phe	Ser	Leu	Ser	Leu	Leu	Gln	Ile	Met	Asp
	50					55					60				
Val	Asp	Glu	Lys	Asn	Gln	Val	Leu	Thr	Thr	Asn	Ile	Trp	Leu	Gln	Met
65					70					75					80
Ser	Trp	Thr	Asp	His	Tyr	Leu	Gln	Trp	Asn	Val	Ser	Glu	Tyr	Pro	Gly
				85					90					95	
Val	Lys	Thr	Val	Arg	Phe	Pro	Asp	Gly	Gln	Ile	Trp	Lys	Pro	Asp	Ile
			100					105					110		
Leu	Leu	Tyr	Asn	Ser	Ala	Asp	Glu	Arg	Phe	Asp	Ala	Thr	Phe	His	Thr
		115					120					125			
Asn	Val	Leu	Val	Asn	Ser	Ser	Gly	His	Cys	Gln	Tyr	Leu	Pro	Pro	Gly
	130						135				140				

Val Ser Lys Asp Phe Ala
500

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 265..1773
- (D) OTHER INFORMATION: /product= "BETA-2 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCCTCCCC TCACCGTCCC AATTGTATTC CCTGGAAGAG CAGCCGGAAA AGCCTCCGCC	60
TGCTCATACC AGGATAGGCA AGAAGCTGGT TTCTCCTCGC AGCCGGCTCC CTGAGGCCCA	120
GGAACCACCG CGGCGGCCCG CACCACCTGG ACCCAGCTCC AGGCGGGCGC GGCTTCAGCA	180
CCACGGACAG CGCCCCACCC GCGGCCCTCC CCCCGGCGGC GCGCTCCAGC CGGTGTAGGC	240
GAGGCAGCGA GCTATGCCCG CGGC ATG GCC CGG CGC TGC GGC CCC GTG GCG	291
Met Ala Arg Arg Cys Gly Pro Val Ala	
1 5	
CTG CTC CTT GGC TTC GGC CTC CTC CGG CTG TGC TCA GGG GTG TGG GGT	339
Leu Leu Leu Gly Phe Gly Leu Leu Arg Leu Cys Ser Gly Val Trp Gly	
10 15 20 25	
ACG GAT ACA GAG GAG CGG CTG GTG GAG CAT CTC CTG GAT CCT TCC CGC	387
Thr Asp Thr Glu Glu Arg Leu Val Glu His Leu Leu Asp Pro Ser Arg	
30 35 40	
TAC AAC AAG CTT ATC CGC CCA GCC ACC AAT GGC TCT GAG CTG GTG ACA	435
Tyr Asn Lys Leu Ile Arg Pro Ala Thr Asn Gly Ser Glu Leu Val Thr	
45 50 55	
GTA CAG CTT ATG GTG TCA CTG GCC CAG CTC ATC AGT GTG CAT GAG CGG	483
Val Gln Leu Met Val Ser Leu Ala Gln Leu Ile Ser Val His Glu Arg	
60 65 70	
GAG CAG ATC ATG ACC ACC AAT GTC TGG CTG ACC CAG GAG TGG GAA GAT	531
Glu Gln Ile Met Thr Thr Asn Val Trp Leu Thr Gln Glu Trp Glu Asp	
75 80 85	
TAT CGC CTC ACC TGG AAG CCT GAA GAG TTT GAC AAC ATG AAG AAA GTT	579
Tyr Arg Leu Thr Trp Lys Pro Glu Glu Phe Asp Asn Met Lys Lys Val	
90 95 100 105	
CGG CTC CCT TCC AAA CAC ATC TGG CTC CCA GAT GTG GTC CTG TAC AAC	627
Arg Leu Pro Ser Lys His Ile Trp Leu Pro Asp Val Val Leu Tyr Asn	
110 115 120	
AAT GCT GAC GGC ATG TAC GAG GTG TCC TTC TAT TCC AAT GCC GTG GTC	675
Asn Ala Asp Gly Met Tyr Glu Val Ser Phe Tyr Ser Asn Ala Val Val	
125 130 135	
TCC TAT GAT GGC AGC ATC TTC TGG CTG CCG CCT GCC ATC TAC AAG AGC	723
Ser Tyr Asp Gly Ser Ile Phe Trp Leu Pro Pro Ala Ile Tyr Lys Ser	
140 145 150	

GCA Ala	TGC Cys	AAG Lys	ATT Ile	GAA Glu	GTA Val	AAG Lys	CAC His	TTC Phe	CCA Pro	TTT Phe	GAC Asp	CAG Gln	CAG Gln	AAC Asn	TGC Cys	771
ACC Thr	ATG Met	AAG Lys	TTC Phe	CGT Arg	TCG Ser	TGG Trp	ACC Thr	TAC Tyr	GAC Asp	CGC Arg	ACA Thr	GAG Glu	ATC Ile	GAC Asp	TTG Leu	819
GTG Val	CTG Leu	AAG Lys	AGT Ser	GAG Glu	GTG Val	GCC Ala	AGC Ser	CTG Leu	GAC Asp	GAC Asp	TTC Phe	ACA Thr	CCT Pro	AGT Ser	GGT Gly	867
GAG Glu	TGG Trp	GAC Asp	ATC Ile	GTG Val	GCG Ala	CTG Leu	CCG Pro	GGC Gly	CGG Arg	CGC Arg	AAC Asn	GAG Glu	AAC Asn	CCC Pro	GAC Asp	915
GAC Asp	TCT Ser	ACG Thr	TAC Tyr	GTG Val	GAC Asp	ATC Ile	ACG Thr	TAT Tyr	GAC Asp	TTC Phe	ATC Ile	ATT Ile	CGC Arg	CGC Arg	AAG Lys	963
CCG Pro	CTC Leu	TTC Phe	TAC Tyr	ACC Thr	ATC Ile	AAC Asn	CTC Leu	ATC Ile	ATC Ile	CCC Pro	TGT Cys	GTG Val	CTC Leu	ATC Ile	ACC Thr	1011
TCG Ser	CTA Leu	GCC Ala	ATC Ile	CTT Leu	GTC Val	TTC Phe	TAC Tyr	CTG Leu	CCA Pro	TCC Ser	GAC Asp	TGT Cys	GGC Gly	GAG Glu	AAG Lys	1059
ATG Met	ACG Thr	TTG Leu	TGC Cys	ATC Ile	TCA Ser	GTG Val	CTG Leu	CTG Leu	GCG Ala	CTC Leu	ACG Thr	GTC Val	TTC Phe	CTG Leu	CTG Leu	1107
CTC Leu	ATC Ile	TCC Ser	AAG Lys	ATC Ile	GTG Val	CCT Pro	CCC Pro	ACC Thr	TCC Ser	CTC Leu	GAC Asp	GTG Val	CCG Pro	CTC Leu	GTC Val	1155
GGC Gly	AAG Lys	TAC Tyr	CTC Leu	ATG Met	TTC Phe	ACC Thr	ATG Met	GTG Val	CTT Leu	GTC Val	ACC Thr	TTC Phe	TCC Ser	ATC Ile	GTC Val	1203
ACC Thr	AGC Ser	GTG Val	TGC Cys	GTG Val	CTC Leu	AAC Asn	GTG Val	CAC His	CAC His	CGC Arg	TCG Ser	CCC Pro	ACC Thr	ACG Thr	CAC His	1251
ACC Thr	ATG Met	GCG Ala	CCC Pro	TGG Trp	GTG Val	AAG Lys	GTC Val	GTC Val	TTC Phe	CTG Leu	GAG Glu	AAG Lys	CTG Leu	CCC Pro	GCG Ala	1299
CTG Leu	CTC Leu	TTC Phe	ATG Met	CAG Gln	CAG Gln	CCA Pro	CGC Arg	CAT His	CAT His	TGC Cys	GCC Ala	CGT Arg	CAG Gln	CGC Arg	CTG Leu	1347
CGC Arg	CTG Leu	CGG Arg	CGA Arg	CGC Arg	CAG Gln	CGT Arg	GAG Glu	CGC Arg	GAG Glu	GGC Gly	GCT Ala	GGA Gly	GCC Ala	CTC Leu	TTC Phe	1395
TTC Phe	CGC Arg	GAA Glu	GCC Ala	CCA Pro	GGG Gly	GCC Ala	GAC Asp	TCC Ser	TGC Cys	ACG Thr	TGC Cys	TTC Phe	GTC Val	AAC Asn	CGC Arg	1443
GCG Ala	TCG Ser	GTG Val	CAG Gln	GGG Gly	TTG Leu	GCC Ala	GGG Gly	GCC Ala	TTC Phe	GGG Gly	GCT Ala	GAG Glu	CCT Pro	GCA Ala	CCA Pro	1491
GTG Val	GCG Ala	GGC Gly	CCC Pro	GGG Gly	ACG Ser	TCA Ser	GGG Gly	GAG Glu	CCG Pro	TGT Cys	GGC Gly	TGT Cys	GGC Gly	CTC Leu	CGG Arg	1539

GAG GCG GTG GAC GGC GTG CGC TTC ATC GCA GAC CAC ATG CGG AGC GAG Glu Ala Val Asp Gly Val Arg Phe Ile Ala Asp His Met Arg Ser Glu 430 435 440	1587
GAC GAT GAC CAG AGC GTG AGT GAG GAC TGG AAG TAC GTC GCC ATG GTG Asp Asp Asp Gln Ser Val Ser Glu Asp Trp Lys Tyr Val Ala Met Val 445 450 455	1635
ATC GAC CGC CTC TTC CTC TGG ATC TTT GTC TTT GTC TGT GTC TTT GGC Ile Asp Arg Leu Phe Leu Trp Ile Phe Val Phe Val Cys Val Phe Gly 460 465 470	1683
ACC ATC GGC ATG TTC CTG CAG CCT CTC TTC CAG AAC TAC ACC ACC ACC Thr Ile Gly Met Phe Leu Gln Pro Leu Phe Gln Asn Tyr Thr Thr Thr 475 480 485	1731
ACC TTC CTC CAC TCA GAC CAC TCA GCC CCC AGC TCC AAG TGAGGCCCTT Thr Phe Leu His Ser Asp His Ser Ala Pro Ser Ser Lys 490 495 500	1780
CCTCATCTCC ATGCTCTTTC ACCCTGCCAC CCTCTGCTGC ACAGTAGTGT TGGGTGGAGG	1840
ATGGACGAGT GAGCTACCAG GAAGAGGGGC GCTGCCCCCA CAGATCCATC CTTTTGCTTC	1900
ATCTGGAGTC CCTCCTCCCC CACGCCTCCA TCCACACACA GCAGCTCCAA CCTGGAGGCT	1960
GGACCAACTG CTTTGTTTTG GCTGCTCTCC ATCTCTTGTA CCAGCCCAGG CAATAGTGTT	2020
GAGGAGGGGA GCAAGGCTGC TAAGTGAAG ACAGAGATGG CAGAGCCATC CACCCTGAGG	2080
AGTGACGGGC AAGGGGCCAG GAAGGGGACA GGATTGTCTG CTGCCTCCAA GTCATGGGAG	2140
AAGAGGGGTA TAGGACAAGG GGTGAAGGG CAGGAGCTCA CACCGCACCG GGCTGGCCTG	2200
ACACAATGGT AGCTCTGAAG GGAGGGGAAG AGAGAGGCCT GGGTGTGACC TGACACCTGC	2260
CGCTGCTTGA GTGGACAGCA GCTGGACTGG GTGGGCCCCA CAGTGGTCAG CGATTCTGTC	2320
CAAGTAGGGT TTAGCCGGGC CCCATGGTCA CAGACCCCTG GGGGAGGCTT CCAGCTCAGT	2380
CCCACAGCCC CTTGCTTCTA AGGGATCCAG AGACCTGCTC CAGATCCTCT TTCCCCACTG	2440
AAGAATTC	2448

(2) INFORMATION FOR SEQ ID NO:14:

(ii) MOLECULE TYPE: protein

Met Ala Arg Arg Cys Gly Pro Val Ala Leu Leu Leu Gly Phe Gly Leu
1 5 10 15

Leu Arg Leu Cys Ser Gly Val Trp Gly Thr Asp Thr Glu Glu Arg Leu
20 25 30

Val Glu His Leu Leu Asp Pro Ser Arg Tyr Asn Lys Leu Ile Arg Pro
35 40 45

Ala Thr Asn Gly Ser Glu Leu Val Thr Val Gln Leu Met Val Ser Leu
50 55 60

$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{y}} \right) = \frac{\partial L}{\partial y}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{z}} \right) = \frac{\partial L}{\partial z}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{\theta}} \right) = \frac{\partial L}{\partial \theta}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{\phi}} \right) = \frac{\partial L}{\partial \phi}$	$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{\psi}} \right) = \frac{\partial L}{\partial \psi}$
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Gly Glu Pro Cys Gly Cys Gly Leu Arg Glu Ala Val Asp Gly Val Arg
 420 425 430
 Phe Ile Ala Asp His Met Arg Ser Glu Asp Asp Asp Gln Ser Val Ser
 435 440 445
 Glu Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Leu Phe Leu Trp
 450 455 460
 Ile Phe Val Phe Val Cys Val Phe Gly Thr Ile Gly Met Phe Leu Gln
 465 470 475 480
 Pro Leu Phe Gln Asn Tyr Thr Thr Thr Thr Phe Leu His Ser Asp His
 485 490 495
 Ser Ala Pro Ser Ser Lys
 500

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) LOCATION: 98..1474
- (D) OTHER INFORMATION: /product= "BETA-3 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGGAACCCC TGTATTTTCT TTTCAAAACC CCCTTTTCCA GTGGAAATGC TCTGTTGTTA	60
AAAAGGAAGA AACTGTCTTT CTGAAACTGA CATCACG ATG CTC CCA GAT TTT ATG	115
Met Leu Pro Asp Phe Met	5
CTG GTT CTC ATC GTC CTT GGC ATC CCT TCC TCA GCC ACC ACA GGT TTC	163
Leu Val Leu Ile Val Leu Gly Ile Pro Ser Ser Ala Thr Thr Gly Phe	20
AAC TCA ATC GCC GAA AAT GAA GAT GCC CTC CTC AGA CAT TTG TTC CAA	211
Asn Ser Ile Ala Glu Asn Glu Asp Ala Leu Leu Arg His Leu Phe Gln	35
GGT TAT CAG AAA TGG GTC CGC CCT GTA TTA CAT TCT AAT GAC ACC ATA	259
Gly Tyr Gln Lys Trp Val Arg Pro Val Leu His Ser Asn Asp Thr Ile	50
AAA GTA TAT TTT GGA TTG AAA ATA TCC CAG CTT GTA GAT GTG GAT GAA	307
Lys Val Tyr Phe Gly Leu Lys Ile Ser Gln Leu Val Asp Val Asp Glu	70
AAG AAT CAG CTG ATG ACA ACC AAT GTG TGG CTC AAA CAG GAA TGG ACA	355
Lys Asn Gln Leu Met Thr Thr Asn Val Trp Leu Lys Gln Glu Trp Thr	85
GAC CAC AAG TTA CGC TGG AAT CCT GAT GAT TAT GGT GGG ATC CAT TCC	403
Asp His Lys Leu Arg Trp Asn Pro Asp Asp Tyr Gly Gly Ile His Ser	100

ATT Ile	AAA Lys	GTT Val 105	CCA Pro	TCA Ser	GAA Glu	TCT Ser	CTG Leu 110	TGG Trp	CTT Leu	CCT Pro	GAC Asp	ATA Ile 115	GTT Val	CTC Leu	TTT Phe	451
GAA Glu	AAT Asn 120	GCT Ala	GAC Asp	GGC Gly	CGC Arg	TTC Phe 125	GAA Glu	GGC Gly	TCC Ser	CTG Leu	ATG Met 130	ACC Thr	AAG Lys	GTC Val	ATC Ile	499
GTG Val 135	AAA Lys	TCA Ser	AAC Asn	GGA Gly	ACT Thr 140	GTT Val	GTC Val	TGG Trp	ACC Thr	CCT Pro 145	CCC Pro	GCC Ala	AGC Ser	TAC Tyr	AAA Lys 150	547
AGC Ser	TCC Ser	TGC Cys	ACC Thr	ATG Met 155	GAC Asp	GTC Val	ACG Thr	TTT Phe	TTC Phe 160	CCG Pro	TTC Phe	GAC Asp	CGA Arg	CAG Gln 165	AAC Asn	595
TGC Cys	TCC Ser	ATG Met 170	AAG Lys	TTT Phe	GGA Gly	TCC Ser	TGG Trp	ACT Thr 175	TAT Tyr	GAT Asp	GGC Gly	ACC Thr	ATG Met 180	GTT Val	GAC Asp	643
CTC Leu	ATT Ile 185	TTG Leu	ATC Ile	AAT Asn	GAA Glu	AAT Asn	GTC Val 190	GAC Asp	AGA Arg	AAA Lys	GAC Asp 195	TTC Phe	TTC Phe	GAT Asp	AAC Asn	691
GGA Gly	GAA Glu 200	TGG Trp	GAA Glu	ATA Ile	CTG Leu	AAT Asn 205	GCA Ala	AAG Lys	GGG Gly	ATG Met 210	AAG Lys	GGG Gly	AAC Asn	AGA Arg	AGG Arg	739
GAC Asp 215	GGC Gly	GTG Val	TAC Tyr	TCC Ser	TAT Tyr 220	CCC Pro	TTT Phe	ATC Ile	ACG Thr	TAT Tyr 225	TCC Ser	TTC Phe	GTC Val	CTG Leu	AGA Arg 230	787
CGC Arg	CTG Leu	CCT Pro	TTA Leu	TTC Phe 235	TAT Tyr	ACC Thr	CTC Leu	TTT Phe 240	CTC Ile	ATC Ile	ATC Ile	CCC Pro	TGC Cys	CTG Leu 245	GGG Gly	835
CTG Leu	TCT Ser	TTC Phe 250	CTA Leu	ACA Thr	GTT Val	CTT Leu	GTG Val 255	TTC Phe	TAT Tyr	TTA Leu	CCT Pro	TCG Ser	GAT Asp 260	GAA Glu	GGA Gly	883
GAA Glu	AAA Lys 265	CTT Leu	TCA Ser	TTA Leu	TCC Ser	ACA Thr	TCG Ser 270	GTC Val	TTG Leu	GTT Val	TCT Ser 275	CTG Leu	ACA Thr	GTT Val	TTC Phe	931
CTT Leu 280	TTA Leu	GTG Val	ATT Ile	GAA Glu	GAA Glu	ATC Ile 285	ATC Ile	CCA Pro	TCG Ser	TCT Ser	TCC Ser 290	AAA Lys	GTC Val	ATT Ile	CCT Pro	979
CTC Leu 295	ATT Ile	GGA Gly	GAG Glu	TAC Tyr	CTG Leu 300	CTG Leu	TTC Phe	ATC Ile	ATG Met	ATT Ile 305	TTT Phe	GTG Val	ACC Thr	CTG Leu 310	TCC Ser	1027
ATC Ile	ATT Ile	GTT Val	ACC Thr 315	GTG Val	TTT Phe	GTC Val	ATT Ile	AAC Asn	GTT Val 320	CAC His	CAC His	AGA Arg	TCT Ser	TCT Ser 325	TCC Ser	1075
ACG Thr	TAC Tyr	CAC His	CCC Pro 330	ATG Met	GCC Ala	CCC Pro	TGG Trp	GTT Val 335	AAG Lys	AGG Arg	CTC Leu	TTT Phe	CTG Leu 340	CAG Gln	AAA Lys	1123
CTT Leu	CCA Pro	AAA Lys 345	TTA Leu	CTT Leu	TGC Cys	ATG Met	AAA Lys 350	GAT Asp	CAT His	GTG Val	GAT Asp 355	CGC Arg	TAC Tyr	TCA Ser	TCC Ser	1171
CCA Pro	GAG Glu 360	AAA Lys	GAG Glu	GAG Glu	AGT Ser	CAA Gln 365	CCA Pro	GTA Val	GTG Val	AAA Lys	GGC Gly 370	AAA Lys	GTC Val	CTC Leu	GAA Glu	1219

AAA AAG AAA CAG AAA CAG CTT AGT GAT GGA GAA AAA GTT CTA GTT GCT Lys Lys Lys Gln Lys Gln Leu Ser Asp Gly Glu Lys Val Leu Val Ala 375 380 385 390	1267
TTT TTG GAA AAA GCT GCT GAT TCC ATT AGA TAC ATT TCC AGA CAT GTG Phe Leu Glu Lys Ala Ala Asp Ser Ile Arg Tyr Ile Ser Arg His Val 395 400 405	1315
AAG AAA GAA CAT TTT ATC AGC CAG GTA GTA CAA GAC TGG AAA TTT GTA Lys Lys Glu His Phe Ile Ser Gln Val Val Gln Asp Trp Lys Phe Val 410 415 420	1363
GCT CAA GTT CTT GAC CGA ATC TTC CTG TGG CTC TTT CTG ATA GTG TCA Ala Gln Val Leu Asp Arg Ile Phe Leu Trp Leu Phe Leu Ile Val Ser 425 430 435	1411
GCA ACA GGC TCG GTT CTG ATT TTT ACC CCT GCT TTG AAG ATG TGG CTA Ala Thr Gly Ser Val Leu Ile Phe Thr Pro Ala Leu Lys Met Trp Leu 440 445 450	1459
CAT AGT TAC CAT TAGGAATTTC AAAAGACATA AGTACTAAAT TACACCTTAG His Ser Tyr His 455	1511
ACCTGACATC TGGCTATCAC ACAGACAGAA TCCAAATGCA TGTGCTTGTT CTACGAACCC	1571
CGAATGCGTT GTCTTTGTGG AAATGGAACA TCTCCTCATG GGAGAAACTC TGGTAAATGT	1631
GCTCATTGTG GGTTGCCATG AGAGTGAGCT GCTTTTAAAG AAAGTGGAGC CTCCTCAGAC	1691
CCCTGCCTTG GCTTTCCCAG ACATTCAGGG AGGGATCATA GGTCCAGGCT TGAGCTCACA	1751
TGTGGCCAGA GTGCACAAAA AGCTGTTGCT ACTTGGTGGA GGAACACCTC CTAGAAGCAG	1811
CAGGCCTCGG TGGTGGGGGA GGGGGGATTC ACCTGGAATT AAGGAAGTCT CGGTGTCTGAG	1871
CTATCTGTGT GGGCAGAGCC TGGATCTCCC ACCCTGCACT GGCTCCTCTG GTGCCG	1927

(2) INFORMATION FOR SEQ ID NO:15:

(11) MOLECULE TYPE: protein

Met	Leu	Pro	Asp	Phe	Met	Leu	Val	Leu	Ile	Val	Leu	Gly	Ile	Pro	Ser
1				5					10					15	
Ser	Ala	Thr	Thr	Gly	Phe	Asn	Ser	Ile	Ala	Glu	Asn	Glu	Asp	Ala	Leu
			20					25					30		
Leu	Arg	His	Leu	Phe	Gln	Gly	Tyr	Gln	Lys	Trp	Val	Arg	Pro	Val	Leu
		35					40					45			
His	Ser	Asn	Asp	Thr	Ile	Lys	Val	Tyr	Phe	Gly	Leu	Lys	Ile	Ser	Gln
	50					55					60				
Leu	Val	Asp	Val	Asp	Glu	Lys	Asn	Gln	Leu	Met	Thr	Thr	Asn	Val	Trp
65					70					75					80
Leu	Lys	Gln	Glu	Trp	Thr	Asp	His	Lys	Leu	Arg	Trp	Asn	Pro	Asp	Asp
				85					90					95	

Ala Leu Lys Met Trp Leu His Ser Tyr His
450 455

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 87..1583
- (D) OTHER INFORMATION: /product= "BETA-4 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCGGCGCTCA CTCGACCGCG CGGCTCACGG GTGCCCTGTG ACCCCACAGC GGAGCTCGCG	60
GCGGCTGCCA CCGGCCCCCG CCGGCCATGA GCGCGCGCGC TTCCCTGGTC CTTTCTCTCC	120
TGGTCGCCCT TTGCGGGCGC GGGAAGTGCC GCGTGCCAA TCGGAGGAA AAGCTGATGG	180
ACGACCTTCT GAACAAAACC CGTTACAATA ACCTGATCCG CCCAGCCACC AGCTCCTCAC	240
AGCTCATCTC CATCAAGCTG CAGCTCTCCC TGGCCAGCT TATCAGCGTG AATGAGCGAG	300
AGCAGATCAT GACCACCAAT GTCTGGCTGA AACAGGAATG GACTGATTAC CGCCTGACCT	360
GGAACAGCTC CCGCTACGAG GGTGTGAACA TCCTGAGGAT CCCTGCAAAG CGCATCTGGT	420
TGCCTGACAT CGTGCTTTAC AACAACGCCG ACGGGACCTA TGAGGTGTCT GTCTACACCA	480
ACTTGATAGT CCGGTCCAAC GGCAGCGTCC TGTGGCTGCC CCCTGCCATC TACAAGAGCG	540
CCTGCAAGAT TGAGGTGAAG TACTTTCCCT TCGACCAGCA GAACTGCACC CTCAAGTTCC	600
GCTCCTGGAC CTATGACCAC ACGGAGATAG ACATGGTCCT CATGACGCCC ACAGCCAGCA	660
TGGATGACTT TACTCCCAGT GGTGAGTGGG ACATAGTGGC CCTCCCAGGG AGAAGGACAG	720
TGAACCCACA AGACCCACG TACGTGGACG TGAATTACGA CTTTCATC ATC AAGCGCAAGC	780
CTCTGTTCTA CACCATCAAC CTCATCATCC CCTGCGTGCT CACCACCTTG CTGGCCATCC	840
TCGTCTTCTA CCTGCCATCC GACTGCGGCG AGAAGATGAC ACTGTGCATC TCAGTGCTGC	900
TGGCACTGAC ATTCTTCCTG CTGCTCATCT CCAAGATCGT GCCACCCACC TCCCTCGATG	960
TGCCTCTCAT CGGCAAGTAC CTCATGTTCA CCATGGTGCT GGTCACTTC TCCATCGTCA	1020
CCAGCGTCTG TGTGCTCAAT GTGCACCACC GCTCGCCCAG CACCCACACC ATGGCACCCCT	1080
GGGTCAAGCG CTGCTTCCTG CACAAGCTGC CTACCTTCCT CTTTCATGAAG CGCCCTGGCC	1140
CCGACAGCAG CCGGCCAGA GCCTTCCCGC CCAGCAAGTC ATGGGTGACC AAGCCCGAGG	1200
CCACCGCCAC CTCCACCAGC CCCTCCAAC TCTATGGGAA CTCCATGTAC TTTGTGAACC	1260
CCGCTCTGCG AGCTTCCAAG TCTCCAGCCG GCTCTACCCC GGTGGCTATC CCCAGGGATT	1320
TCTGGCTGCG GTCTCTGGG AGGTTCCGAC AGGATGTGCA GGAGGCATTA GAAGGTGTCA	1380

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Creation date: 11-12-2003

Indexing Officer: TBARA - TIBERIOUS BARA

Team: OIPEBackFileIndexing

Dossier: 09703951

Legal Date: 01-30-2001

No.	Doccode	Number of pages
1	CTMS	1

Total number of pages: 1

Remarks:

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